Amendments to the Specification:

Please replace paragraph **[0008]** with the following paragraph:

The present invention is directed to the sequential identification of linked molecules in a polymer, such as nucleotide bases of a nucleic acid, by passing the polymer through a nanometer-scale channel formed between a pair of nanoelectrodes. Variation and/or modulation of a bias voltage applied across the nanoelectrodes and subsequent signal processing allows derivation of an electronic characteristic feature or signal that may be compared to known values of the characteristic signal that correspond to desired molecules of interest. The comparison results in the identification of the polymer's molecules in sequence. In the description of the invention provided below, reference is made specifically to preferred embodiments wherein the polymer being sequenced is preferably a nucleic acid, such as a single or double stranded DNA base, however the invention is not meant to be limited to such polymers.

Please replace paragraph **[0018]** with the following paragraph:

In another aspect, the present invention provides an apparatus for performing the above studies, comprised of the pair nanoelectrodes to which is connected a signal generator for applying and modulating (and optionally varying) a bias voltage corresponding to one or more energy differences between the internal energy levels of a molecule of interest, a means for urging the polymer through the nanoelectrode channel, and signal processing means for acquiring the tunneling current signal, coherently demodulating the acquired signal and comparing the resultant characteristic electrical signal to known values of the signal associated with known molecules. In optional embodiments, a nanopore or nanochannel may be proximate to the nanoelectrodes so as to restrict the passage of the polymer through the channel to a single molecule at a time. As discussed above, optical tweezers, an electric field generator, or other urging means may be used to force the polymer through the nanoelectrode channel, and filters may be used to improve the signal to noise ratio of the acquired signal.

Please replace paragraph **[0021]** with the following paragraph:

For a better understanding of the present invention, reference is made to the accompanying drawing and detailed description, wherein:

Please replace paragraph **[0025]** with the following paragraph:

The present invention provides systems and methods for sequencing polymers. With reference to **Figure 1** (which is not drawn to scale), a preferred embodiment of the present invention involves urging the polymer **2** in solution across a channel **4** between a pair of nano-electrodes **6** one molecule **8** at the time, and using a conventional signal generator **10** to center a bias voltage V_{BI} **12** across the electrodes **6** that corresponds to the energy difference between any two of the internal energy levels of the molecule **8** of interest. A modulation waveform W_{MOD} **14** is then applied to the bias voltage V_B **12**. A tunneling current $I_{TUNNELING}$ **16** traversing the channel **4** through the molecule **8** is acquired by a sensor **18** (*e.g.*, a current sensor) and relayed to signal processing equipment **20**, which can include a lock-in amplifier and/or phase sensitivity detector. The acquired tunneling current I_T **16** is then demodulated by demodulator **22** in order to derive a characteristic signal S_C **24** ($\frac{d^n I_T}{dV_B^n}$) that can then be compared to a predetermined signal S_{KNOWN} **26** associated with a known molecule for a determination whether the molecule **8** traversing the channel **4** is identical to the known molecule. The acquired tunneling current I_T **16** may optionally be passed to a either a band pass or low pass filter **28**, respectively, before or after demodulation. Conventional techniques can be employed to accomplish the comparison of the derived characteristic signal S_C **24** to the predetermined signal S_{KNOWN} **26**, such as through linear and/or non-linear curve-fitting and/or variation analyses (*e.g.*, Allan Deviation.)

Please replace paragraph **[0026]** with the following paragraph:

With reference to **Figure 2**, the polymer **2** may be any type of polymer known in the art, but preferably comprises a nucleic acid or a protein. DNA is a polymer of deoxyribonucleotides, which are comprised of deoxyribose, one or more phosphate groups, and a derivatives of adenine (A), guanine (G), thymine (T) and cytosine (C). The genetic information of a DNA strand **3** can be determined by sequencing the four distinct bases (A, G, C, and T) in the strand **3**. RNA may also be sequenced, recognizing that RNA strands include uracil (U) molecules instead of thymine among the four bases. The DNA strand may be single-stranded or double-stranded, and known techniques may be applied to reduce an initially double-stranded sample to a single stranded and/or to eliminate secondary DNA structures. For convenience, any conventional method may be employed to dissociate a double-stranded

DNA strand into single-stranded, such as by disrupting the hydrogen bonds between paired bases with heat or ionizing acids or alkalis.

Please replace paragraph **[0041]** with the following paragraph:

There is no limit known to the inventors on the length of polymer that can be sequenced employing the present invention, however, the present invention provides optimal results when the polymer being sequenced has a linear, curved or straight backbone, as difficulties may be encountered in the optional step of straightening (*i.e.*, funneling) the polymer if the polymer has too irregular a shape. The desire for an optimal throughput will also pragmatically limit how slowly the polymer will be sequenced -- slower speeds will produce better signal to noise ratios, but at the lowest speed limits Brownian motion will generate ambiguities. Thus, the urging method~~driving field~~ should be selected to eliminate Brownian motion effects and increase throughput.